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Result
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
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1: geneseqp1980s:*
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3: geneseqp2000s:*
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Match
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Gapop 10.0 , Gapext 0.5
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684
2105692 seqs, 386760381 residues
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geneseqD2001s:*
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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                                               AAB85347
AAG89145
AAU83605
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effective than previous contraceptive vaccines which only caused 75%

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{ <b>₽</b> }	IAAD)	-) UNIV		VIRGIN	VIRGINIA PATENT	TEN	T FOUND.			
\$ P }	Hao 2	, Herr		JC, i	Jayes	FĽ,	Shetty J, Wolkowicz MJ;			
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777	New h	nan ept	sperm	rm sur vacci	surface accines.	pro	proteins C7/8, SAMP32 and C58	for devel	development	o Ff
\$ 8 \$	Claim	ö	Page	-09	61; 63	βpp;	English.			
និក	The i	Ž Č	ion	relat	es to	e po	vel human sperm specific survicins, nucleic acids enco	urface pro	eins,	
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Best Local S
Matches 124
                        gene expression by rectifying mutations or deletions in a patient's genome that affect the activity of GENSET or by supplementing the patients own production of GENSET polypeptides. Conversely, antisense nucleic acid molecules may be administered to down regulate GENSET expression by binding with the cells' own genes and preventing their expression. The sense and antisense nucleic acids may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acid sequences in samples, and hence to determine which
                                                                                                                                        The invention relates to full length GENSET human nucleic acids encoding potentially secreted proteins. For nucleic acids and the polypeptides they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate GENSET gene expression. For example, they be used to treat disorders associated with decreased GENSET can expression to used to treat disorders associated with decreased GENSET.
                                                                                                                                                                                                                                                          Full length GENSET human nucleic acids encoding potentially secreted proteins, useful in gene therapy and vaccination against a variety of diseases, and for diagnosis of those diseases.
            patients
                                                                                                                                                                                                                                  Claim
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06-MAR-2000; 2000US-0187470P
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                                                                                                                                                                                                                                 21; Page 807; 921pp; English.
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Pred. No. 2.3e-54;
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28-NOV-2000;
01-DEC-2000;
20-DEC-2000;
20-DEC-2000;
20-DEC-2000;
28-FEB-2001;
01-MAR-2001;
110-MAY-2001;
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25-JUL-2000
25-JUL-2000
26-JUL-2000
28-JUL-2000
01-AUG-2000
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23-AUG-2000
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Pred. No. 2.3e-54;
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Best Local (
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                                                                                                                                                                                                                                             Human; secreted protein; zuparl; inflammation; immunosuppressive; cancer; tissue remodelling; vaccine; autoimmune disease; cell-mediated immunity; fibrinolysis cosquiation; circulatory anomaly; wound healing; valinerary; contraception; sperm motility; fertilisation; immunocontraceptive;
                                                                                                                                                                                                                                                                                                                                                                                                 Human secreted protein, zuparl.
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Grimaldi JC,
                                  Peptide
                                                                                                                              Homo sapiens
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C, Gurney AL,
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Location/Qualifiers
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Smith V, Stephan JF, Watanabe CK, Wood WI;
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Pred. No. 2.3e-54;
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The present invention relates to a novel human secreted protein CC designated zuparl and its nucleic acid. zuparl gene is used in gene CC therapy and is located on chromosome 19q.13.2. Zuparl is useful in CC competing with complement or other membrane targetted complexes in CC reducing inflammation, coagulation or tissue remodeling and for treating CC autoimmune diseases, circulatory anomalies and blocking tissue remodeling CC in aggressive cancers, and used in wound healing. Zuparl is used in CC applications related to fibrinolysis coagulation, remodeling wound CC healing, contraception and fertility. Zuparl are useful in enhancing CC viability of cryopreserved sperm, as a component in acrosome reaction, CC enhancing sperm motility and enhancing egg-sperm interactions and is CC useful for enhancing fertilisation during assisted reproduction in humans CC and in animals by preventing attack by complement. In cases where CC pregnancy is not desired, zuparl may function as germ-cell-specific CC antigens for use as components in memunocontraceptive or anti-fertility vaccines to induce formation of antibodies to selectively inhibit a cell-mediated immunity. Zuparl are useful as markers for testis tissue or CC mediated immunity. Zuparl are useful as markers for testis tissue or CC gearn and as components of defined cell culture media to replace serum. CC cell populations, inactivating zuparl and rendering the cells susceptible coll spoins by inhibiting components of spermatogenesis and/or sperm activation and used for contraception in domestic animals and livestock.

The present escapence is human zuparl protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel zupar1 polypeptide useful for reducing inflammation, enhancing viability of cryopreserved sperm, sperm motility, egg-sperm interactions, and fertilization, or as components in antiinfertility vaccines.
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Disulfide-bond
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                                is human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Membrane associated domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Beta strand"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Presnell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           strand"
                               zuparl protein
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Query Match

100.0%;

Score

684;

DB 5

Length 124;

Sequence

124

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AAU83232
ID AAU8
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                                                                                 The invention describes an isolated mammalian secreted polypeptide (MSP) (C (I). (I) is useful to direct the secretion of other proteins of interest from a host cell, to monitor secretion of proteins, to degenerate sequences comprising all nucleotide sequences encoding a particular (C polypeptide, to screen for cell metabolism effecting receptors, for (identifying new target receptors and drug design, for identifying, for (identifying new target receptors and drug design, for identifying, for (identifying) for 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ঠ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 12; Page 382-383; 397pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated mammalian secreted polypeptide useful in therapeutic and diagnostic methods, to direct secretion of other proteins of interest from host cell, as educational tools, and as laboratory practicum kits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sheppard PO,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU83232 standard; protein; 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein secretion; mammalian secreted polypeptide; MSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                  mammalian secreted polypeptide, described in the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2002-147999/19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INKGCLRATSCGLEEPVSYRGVTYSLTTNCCTGRLCNRAPSSQTVGATTSLALGLGMLLP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MVLCWLLLLLVMALPPGTTGVKDCVFCELTDSMQCPGTYMHCGDDEDCFTGHGVAPGTGPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRLL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRLL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MVICWILLILVMALPPGTTGVKDCVFCELTDSMQCPGTYMHCGDDEDCFTGHGVAPGTGPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Presnell SR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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; Mismatches 0;
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Sequence 124 AA,

Query Match Best Local Similarity

100.0%;

Score Pred.

684; DB 6; No. 2.3e-54;

Length

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RESULT 6
ABU80752
ID ABU8
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Best Local &
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                                              The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides and polynucleotides are useful for preparing a medicament useful in the diagnostis and treatment of tumours. Anti-PRO antibodies are useful in diagnostic assays for PRO, by detecting its expression in specific cells, tissues or serum, and for affinity purification of PRO from recombinant cell culture or natural sources. ABU80739-ABU80860 represent the human PRO polypeptides of the invention. Note: The sequence data for this patent was obtained in electronic format directly from the USPTO web site at seqdata.uspto.gov/psipsDIDEntry.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001;
29-JUN-2001;
09-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Baker KP,
Grimaldi
Sequence 124
                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; Fig 28; 314pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for the manufacture of a medicament for diagnosing or treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; ACA66854.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-342045/32
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01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; PRO polypeptide; secreted and transmembrane protein; anti-PRO antibody; diagnostic assay; gene expression; tumour; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human PRO polypeptide #14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
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C, Gurney AL,
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ilarity 100.0%;
Conservative (
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Pred. No. 2.3e-54;
Mismatches 0;
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The invention describes an isolated nucleic acid molecule comprising a sequence with at least 80% identity to: (a) a nucleotide encoding any of 122 PRO (secreted and transmembrane) polypeptides whose sequences are fully defined in the specification; or (b) any of 122 nucleotide sequences having e.g. 4834, 2504 or 1759 bp fully defined in the specification; or the full length coding sequence of any these 122 nucleotide sequences. The PRO polypeptides or polynucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These are particularly useful for detecting tumours (e.g. lung tumour, colon tymour, breast tumour, prostate tumour, rectal tumour, or liver tumour) in a mammal, for stimulating the release of TNP-alpha from human blood, for stimulating the proliferation or differentiation of chondrocyte cells, for stimulating proliferation of pericyte cells, or for modulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New genes, and its encoded secreted and transmembrane polypeptides, useful for stimulating Tumor Necrosis Factor alpha, or chondrocyte or pericyte proliferation, especially for treating lung tumors, arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Grimaldi JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Baker KP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human secreted and transmembrane protein PRO9862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AB033718;
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JC, Gurney
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Smith V, Stephan JF, Watanabe
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tanabe CK, Wood WI;
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Best Local S
Matches 124
                                                                                                                                                                                                                                                                                          25-JUL-2000;
01-JUN-2001;
29-JUN-2001;
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                                                                                                                                   Baker KP,
Grimaldi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; secreted and transmembrane protein; PRO; cardiant; cytostatic; antiangiogenic; hypotensive; vulnenry; antiarteriosclerotic; gene therapy; cardiovascular disorder; endothelial disorder; angiogenic disorder; cardiac hypertrophy; trauma; cancer; age-related macular degeneration; atherosclerosis; hypertension; arterial restenosis; rheumatoid arthritis; angina; myocardial infarctic thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma;
                                                  WPI; 2003-393229/37.
N-PSDB; ACA68510.
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C, Gurney
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2001WO-US017800.
2001WO-US021066.
2002US-00119480.
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Pred. No. 2.3e-54;
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                                                                                                               A, C. Watanabe
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One hundred and eighty seven nucleic acids encoding PRO polypeptides,

useful in

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Best Local Similarity
Matches 124; Conser
                                                                                                                                                                                                                                                                   Baker KP,
Grimaldi
                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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                               New nucleic acid encoding for a PRO protein, useful for the manufacture of a medicament for diagnosing or treating tumors or for measuring or detecting expression of an associated gene.
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                                                                                                                                                                     N-PSDB;
                                                                                                                                                                                                        WPI;
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                                                                                                                                                                                                                                                                                                                                                                       (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABJ72241 standard; protein; 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention describes one hundred and eighty seven nucleic acids encoding novel human secreted and transmembrane (PRO) polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
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                                                                                                                                                                  2003-521818/49.
DB; ABT44239.
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erentiation; dermal fibroblast; tumour; gene therapy; cytostatic.
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IC, Gurney
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Smith V,
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Pred. No. 2.3e-54;
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                                                                                                                                                                                                                                                               ME, Goddard A, Godow
Stephan JF, Watanabe
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canabe CK, Wood
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Best Local S
Matches 124
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29-JUN-2001;
09-APR-2002;
                                                                                                                    Baker KP,
Grimaldi
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            New PRO protein encoding nucleic acid, useful for preparing polypeptides and anti-PRO antibodies for detecting the presetumor in a mammal.
                                                                         N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                              PRO; blood; proliferation; pericyte cell; TNF alpha; chondrocyte; tumour necrosis factor; proliferation; differentiation; gene ther dermal fibroblast.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Human PRO9862
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2001WO-US021066.
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                                                                                                                  Gerritsen ME, Goddard Smith V, Stephan JF,
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Pred. No. 2.3e-54;
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                                                                                                                     A, Godows
Watanabe
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Claim 11;

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                                                                                                                New transmembrane polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, in chromosome identification, chromosome markers, or in generating probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001; 2001WO-US017800
29-JUN-2001; 2001WO-US021066
09-APR-2002; 2002US-00119480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human secreted/transmembrane polypeptide PRO 9862.
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                                                             Claim 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                   (GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                             JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                purification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRLL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MVLCWLLLLVMALPPGTTGVKDCVFCELTDSMQCPGTYMHCGDDEDCFTGHGVAPGTGPV
                                                          Fig 28; 315pp; English.
                                                                                                                                                                                                                                                                                                                          Desnoyers
C, Gurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein; 124
                                                                                                                                                                                                                                                                                                                       ¥£,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                             Gerritsen
Smith V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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Pred. No. 2.3e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B
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                                                                                                                                                                                                                                                                                                                             ME, Goddard A, Godowski PJ;
Stephan JF, Watanabe CK, W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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The invention relates to an isolated nucleic acid encoding a PRO

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RESULT 12
ABJ72071
ID ABJ72
XX ABJ72
XX ABJ72
XX ABJ72
XX ABJ72
XX Human
XX Human
XX Human
XX recep
XX recep
XX recep
XX recep
XX 29-AU
PF 29-AU
PF 29-JU
PR 24-FE
PR 01-JU
PR 29-JU
PR 39-JE
PR 01-JU
PR 29-JU
PR 29-JU
PR 29-JU
PR 29-JU
PR 29-JU
PR 29-JU
PR 39-JE
PR 01-JU
PR 29-JU
PR 39-JE
PR 01-JU
PR 39-JU
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Best Local
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24-FEB-2000; 2000WO-US005004.
02-MAR-2000; 2000WO-US005841.
01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
                                                                                         Baker KP,
Grimaldi :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; PRO; membrane bound protein; membrane bound recept cell proliferation; cell migration; cell differentiation; mitogenic factor; survival factor; cytotoxic factor; differentiation factor; neuropeptide; hormone; cell recept receptor-ligand interaction; cytostatic; chondrocyte; tum
   WPI; 2003-522018/49.
N-PSDB; ABT43895.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-AUG-2002; 2002US-00232224.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-APR-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human membrane bound receptor/protein PRO9862 amino acid sequence
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                                                                                                                                                                                  (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MYLCWLLLLYWALPPGTTGVKDCVFCELTDSMQCPGTYMHCGDDEDCFTGHGVAPGTGPV
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                                                                                         Desnoyers L,
C, Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                         Gerritsen ME, Goddard A, Godows
Smith V, Stephan JF, Watanabe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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Pred. No. 2.3e-54;
Mismatches 0;
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                                                                                               Godowski PJ;
tanabe CK, Wood
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cc encoding human PRO membrane bound proteins or receptors. Extracellular committee play important roles in the formation, differentiation and cc maintenance of multicellular organisms. The fate of many individual cells cc (for example proliferation, migration or differentiation) is typically cc governed by information received from other cells and the immediate centromment. The information is often transmitted by secreted compironment, the information is often transmitted by secreted compironment, the information is often transmitted by secreted compironments, differentiation factors, neuropeptides and hormones) which are crecived and interpreted by diverse cell receptors may be of use as pharmaceutical and diagnostic agents, such as in the blocking of receptor of comparts of novel human membrane bound receptors and proteins, along that the cDNA sequences encoding them. The novel proteins of the invention may have cytostatic activities through the stimulation of commitacture of a medicament for diagnosing or treating a tumour in a membrane bound receptor membrane of the invention may be useful for the condition, they may be useful for measuring or detecting the corression of a tumour associated gene. The present sequence is the amino acid acid sequence of a human PRO protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                  human; secreted and transmembrane protein; PRO; cytostatic; vul antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell differentiation; tumour necrosis factor alpha (TNF)-alpha release; dermal fibroblast cell proliferation; lunguermal fibroblast cell differentiation inhibitor; tumour; lunguermal fibroblast cell differentiation inhibitor;
                           17-APR-2003
                                                                                                                                                                                                                                                           colon tumour; breast tumour; prostate tumour; rectal tumour;
liver tumour; tissue typing; chromosome mapping; gene mappin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human secreted and transmembrane protein PRO9862.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for the manufacture of a medicament for diagnosing or treating
                                                                                          US2003073814-A1
                                                                                                                                                            Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADB83518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADB83518 standard; protein; 124 AA.
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                                                                                                                                                         sapiens
                                                                                                                                                                                                                           therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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100.0%; Pr
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Pred. No. 2.3e-54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytostatic; vulnerary;
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                                                                                                                                                                                                                                                           CC for stimulating the proliferation or differentiation of chondrocyte cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide cells. PRO231, PRO357, PRO725, PRO1306 or PRO1419 polypeptide cells. PRO231, PRO357, PRO725, PRO1306 or PRO1419 polypeptide cells. PRO2414, PRO1306, PRO340, PRO360, PRO360, PRO360, PRO360, PRO1306, PRO1411, PRO1309, CC PRO1478, PRO11314, PRO1266, PRO363, PRO531, PRO1083, PRO1411, PRO1309, CC PRO1255, PRO1181, PRO1126, PRO1195, PRO1977, PRO1411, PRO1309, CC PRO1286, PRO1330, PRO1347, PRO1305, PRO1973, PRO1274, PRO1412, PRO1330, PRO1347, PRO1305, PRO1373, PRO1279, PRO1340, PRO1338, CC PRO1887, PRO1298, PRO1347, PRO1409, PRO1373, PRO1279, PRO1344, PRO4222, PRO1887, PRO1328, PRO1347, PRO1409, PRO1373, PRO1279, PRO1344, PRO4222, PRO1887, PRO1329, PRO9836 or PRO10096 polypeptide are useful for cells. PRO1360, PRO1373, PRO1468, PRO4302, PRO4408, PRO1311, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408, PRO5723, PRO7525, PRO7154, or PRO7425, polypeptide are useful for cells. PRO5725, PRO7154, or PRO7425, polypeptide are useful for cells. PRO5725, PRO7154, or PRO7425, polypeptide are useful for cells. PRO5725, PRO7154, pRO5727, PRO1488, PRO4302, PRO4408, PRO5723, PRO5725, PRO7154, or PRO7425, polypeptide are useful for cells. PRO5724, PRO7174, PRO5778, PRO4302, PRO4408, PRO5723, PRO5725, PRO7154, PRO5725, PRO7174, PRO5778, PRO4302, PRO4408, PRO5725, PRO7154, PRO5725, PRO7174, PRO5778, PRO4302, PRO4408, PRO5725, P
                                                                                                                                                                      Matches 124;
                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                           Sequence 124 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention describes an isolated PRO (secreted and transmembrane) polypeptide (I). PRO982, PRO1160, PRO1187 or PRO129 polypeptide are useful for stimulating the proliferation of or gene expression in pericyte cells. PRO357, PRO329, PRO1272 or PRO4405 polypeptide are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New PRO polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, chromosome identification, tissue typing, or as hybridization probes in chromosome and gene mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-644806/61.
N-PSDB; ADB83517.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11; Fig 28; 315pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-AUG-2002; 2002US-00218849
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                                                                                                                                                                                            Local Similarity
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                                                                                                         MVLCWLLLLVMALPPGTTGVKDCVFCBLTDSMQCPGTYMHCGDDBDCFTGHGVAPGTGPV
INKGCLRATSCGLEEPVSYRGVTYSLTTNCCTGRLCNRAPSSQTVGATTSLALGLGMLLP
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C, Gurney
                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                      PRO
                                                                                                                                                                                                                                                                                                  polypeptide.
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Smith V, Ste
                                                                                                                                                                        0
                                                                                                                                                                    Score 684; DB 7;
Pred. No. 2.3e-54;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ME, Goddard A, Godowski
Stephan JF, Watanabe CK,
                                                                                                                                                                                                                 Length 124;
                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Godowski PJ;
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                                                                                                                                                                      Gaps
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121

PRLL

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PRLL

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RESULT 14
ADB80624
ADB80624
AC ADB8
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The invention describes an isolated PRO (secreted and transmembrane) CC polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are CC useful for stimulating the proliferation of or gene expression in CC pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful for stimulating the proliferation of differentiation of chondrocyte cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide are useful for stimulating the release of tumour necrosis factor (TNF)-ce alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO1244, PRO1274, PRO1411, PRO1411, PRO14112, PRO1247, PRO1357, PRO1244, PRO1309, PRO1273, PRO1274, PRO1417, PRO14112, PRO1243, PRO1336, PRO1347, PRO1305, PRO1273, PRO1273, PRO1367, PRO1367, PRO1367, PRO1367, PRO1367, PRO1369, PRO1474, PRO1379, PRO1367, PRO1369, PRO1379, PRO1376, PRO1367, PRO1367, PRO1369, PRO1373, PRO1379, PRO1379, PRO1376, PRO1367, PRO1367, PRO1369, PRO1373, PRO1377, PRO1474, PRO1377, PRO1476, PRO1367, PRO1369, PRO1379, PRO1369, PRO1369, PRO1373, PRO3543, PRO3543, PRO3543, PRO3543, PRO3543, PRO3543, PRO3567, PRO1567, PRO1667, PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           One hundred and twenty two nucleic useful in gene therapy, chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ADB80623.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Baker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2003088068-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hybridization probes in chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          colon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour; tissue typing; chromosome mapping; gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TNF)-alpha release; dermal fibroblast cell proliferation; leng fibroblast cell differentiation inhibitor; tumour; lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2003-657982/62.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in gene therapy,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fig 28; 305pp;
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C, Gurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         secreted and transmembrane protein PRO9862
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Smith V, Stephan JF, Watanabe CK, W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acids encoding PRO polypeptides, identification, tissue typing, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and gene mapping.
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RESULT 15
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Best Local
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                                                                                Baker KP,
Grimaldi
                                                                                                                                                    01-JUN-2001; 2001WO-US017800
29-JUN-2001; 2001WO-US021066
09-APR-2002; 2002US-00119480
                                                                                                                                                                                                                                                                                                                                      Chondrocyte cell differentiation; tumour necrosis factor alpha (TNP) alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung colon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour; tissue typing; chromosome mapping; gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nove1
                                                                                                                                                                                                                                                                                                                                                                                                                 human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell proliferation;
                                        N-PSDB;
                                                                                                                                                                                                             29-AUG-2002; 2002US-00232223
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                                                                                                                                                                                                                                                                                                  Homo
                                                                                                                                                                                                                                                                                                                               gene
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                                      2003-765525/72.
DB; ADB73164.
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C, Gurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            secreted and transmembrane protein PRO9862
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein; 124
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                                                                                Gerritsen ME, Goddard A, Godowski Smith V, Stephan JF, Watanabe CK,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 684; DB 7;
Pred. No. 2.3e-54;
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                                                                            Godowski PJ;
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                                                                                                                                                                                                                                                                                                                                                                            tumour;
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New isolated PRO polypeptides useful as molecular weight markers in protein electrophoresis, useful for tissue typing, and for treating

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC Pholypeptide (I). PRO392, PRO1160, PRO1187 or PRO1329 polypeptide are useful for stimulating the proliferation of or gene expression in certificating the proliferation of or gene expression in pericyte cells. PRO357, PRO229, PRO1272 or PRO405 polypeptide are useful CC for stimulating the proliferation or differentiation of chondrocyte cells. PRO317, PRO357, PRO725, PRO1127 or PRO405 polypeptide are useful CC ealpa from human blood. PRO369, PRO1106 or PRO1419 polypeptide CC alpha from human blood. PRO362, PRO357, PRO725, PRO1130, PRO1419, PRO214, PRO377, PRO377, PRO377, PRO1063, PRO1419, PRO1419, PRO1131, PRO1136, PRO1136, PRO1192, PRO11274, PRO1374, PRO1375, PRO1126, PRO1126, PRO1127, PRO1274, PRO1374, PRO1375, PRO1136, PRO1187, PRO1274, PRO1374, PRO1375, PRO1328, PRO4341, PRO1183, PRO11279, PRO1274, PRO1338, PRO1288, PRO4341, PRO1180, PRO1474, PRO1377, PRO1387, PRO1388, PRO4322, PRO4887, PRO3387, PRO1387, PRO1388, PRO4322, PRO4887, PRO3387, PRO1388, PRO4333, PRO3444, PRO4322, PRO4887, PRO1388, PRO4331, PRO33844, PRO4322, PRO4887, PRO1989, PRO1994, PRO17272, PRO1488, PRO4322, PRO4887, PRO1994, PRO1994, PRO17272, PRO1488, PRO4322, PRO4887, PRO1994, PRO1994, PRO19772, PRO1488, PRO43027, PRO4408, PRO5778, PRO5778, PRO1994, PRO1994, PRO1974, PRO5778, PRO4332, PRO4887, PRO1994, PRO1994, PRO1974, PRO5778, PRO4332, PRO4887, PRO1994, PR
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Matches 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; Fig 28; 308pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transmembrane PRO polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                            121
                                                                                                121 PRLL 124
                                                                                                                                                                                         tch 100.0%; Score 684; DB 7; Length 124; al Similarity 100.0%; Pred. No. 2.3e-54; 124; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                        1 MVLCWLLLLVMALPPGTTGVKDCVFCELTDSMQCPGTYMHCGDDEDCFTGHGVAPGTGPV
1 MVLCWLLLLVMALPPGTTGVKDCVFCELTDSMQCPGTYMHCGDDEDCFTGHGVAPGTGPV
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OM protein - protein search, using sw model
April 15, 2005, 14:00:50; Search time 184 Seconds (without alignments) 345.097 Million cell updates/sec
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Title:
Perfect score:
Sequence: US-10-809-654-16 684

Run on:

1 MVLCWLLLLVMALPPGTTGV......VGATTSLALGLGMLLPPRLL 124

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt\_03:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

			1	,	!!!!!!	
ະ	87.5	12.8	118	N	Q9NCQ7	Q9ncq7 dendroides
ພັ	87	12.7	166	N	Q8K1T6	Q8k1t6 mus muscu
4	86.5	12.6	126	μ	LY6E CHICK	Q90986 gallus
ັ້	86	12.6	294	N	Q9GYJ3	
ğ	98	12.6	346	N	095274	O95274 homo sapier
7	86	12.6	346	N	Q9UJ74	Q9uj74 homo sapier
8	85.5	12.5	560	N	Q9U013	Q9u013 giardia
9	85.5	12.5	966	N	Q22378	~
ö	84.5	12.4	123	N	Q9NCQ9	Q9ncq9 dendroides
Ë	84.5	12.4	123	N	Q9D7U0	_
Ñ	84.5	12.4	136	N	Q9NCR2	Q9ncr2 dendroides
ω	84.5	12.4	474	N	Q68EF1	Q68ef1 mus musculu
4	84	12.3	119	N	Q64HX7	Q64hx7 oncorhynch
5	84	12.3	201	N	Q9PTC7	Q9ptc7 oxyuranus m

## ALIGNMENTS

RRRR	22232	Z Z Z Z	Z Z Z Z Z	****	RARAKARRE	**************************************	QRTDM5
TISSUE=BRAIN; Strausberg R.; Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).	n E.D., Dickson M. z J., Myers R.M., s D.E., Schnerch A	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne F.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heleh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,	J. Biol. Chem. 278:30506-30515(2003).  [2] SEQUENCE FROM N.A.  TISSUE=Brain; MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Klausner R.D., Collins F.S., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  PISSUB=Testis;  MEDLINE=22791710; PubMed=12788941; DOI=10.1074/jbc.M301713200;  Shetty J. Wolkowicz M.J., Digilio L.C., Klotz K.L., Jayes F.L.,  Diekman A.B., Westbrook V.A., Farris E.M., Hao Z., Coonrod S.A.,  Flickinger C.J., Herr J.C.;  Flickinger C.J., Herr J.C.;  "SANE14, a novel, acrosomal membrane-associated,  "SANE14, a novel, acrosomal membrane-associated,  glycosylphosphatidylinositol-anchored member of the Ly-6/urokinase- type plasminogen activator receptor superfamily with a role in sperm- edg interaction.";	M5  Q8TDM5  Q8TDM5  Q8TDM5;  PRELIMINARY;  PRT; 124 AA.  Q8TDM5;  O1-JUN-2002 (TrEMBLrel. 21, Created) O1-JUN-2002 (TrEMBLrel. 21, Last sequence update)  25-QCT-2004 (TrEMBLrel. 28, Last annotation update)  Sperm acrosomal membrane protein 14 (SPACA4).  Name-SAMP14; Synonyms-SPACA4; ORFNames-UNQ3046; Homo sapiens (Human).  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.  NCBI_TaxID=9606;

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RESULT

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                                     RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetcw K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetcw K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsiah F.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Robards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Alones S. T. Marra M. A.
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bioinformatics assessment.";
Genome Res. 13:2265-2270(2003).
EMBL; AF353721; AAL83950.1; -.
EMBL; BC047334; AAH47334.1; -.
EMBL; BC047334; AAQ88753.1; -.
EMBL; AY358387; AAQ88753.1; -.
Genew; HGNC:16441; SPACA4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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RIKEN cDNA 1700008E09.
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MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
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Rodentia;
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Matches 84
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Testis;
STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Konno Y. - Arian and subtraction of cap-trapper-selected cDNAs
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAINS-C57BL/GJ; TISSUE-Testis;
MEDLINE-99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                   the RIKEN Genome Exploration Research Group "Analysis of the mouse transcriptome based c 60,770 full-length cDNAs.";
Nature 420:563-573(2002)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus adult
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01-JUN-2002
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                                                                                                                                                         The FANTOM Consortium,
                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences.'
Proc. Natl. Acad. Sci. U.S
                                                                                                                                                                                                           Nature 409:685-690(2001).
                                                                                                                                                                                                                                  RIKEN FANTOM Consortium;
                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=1700008E09Rik;
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                                                                                                                                                                                                                       "Functional annotation of a full-length mouse
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2001 (TrEMBLrel. 17, Last sequence update)
2002 (TrEMBLrel. 21, Last annotation update)
2002 (TrEMBLrel. 21, Last annotation update)
2010 adult male testis CDNA, RIKEN full-length enriched
21 clone:1700008E09 product:hypothetical protein, full ins
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Rodentia; Sciurognathi; Muridae;
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2 STRAIN-C57BL/61; TISSUE-Testis;

2 STRAIN-C57BL/61; TISSUE-Testis;

3 Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,

4 Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,

5 Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Turuno M.,

6 Arakawa T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,

7 A Imotani K., Ishi Y., Itoh M., Izawa M., Kasukawa T., Kato H.,

8 A Imotani K., Ishi Y., Konno H., Kouda M., Koya S., Kurihara C.,

8 A Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,

8 A Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,

8 A Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai K.,

9 A Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai K.,

9 A Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai K.,

9 A Okazaki Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,

10 A Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,

11 A Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,

12 A Muramateu M., Hayashizaki Y., Yasunishi A., Yoshida K., Yoshino M.,

13 A Wuramateu M., Hayashizaki Y., Saito H., Yoshida K., Yoshino M.,

14 A Matsurated (JUL-2000) to the EMBL/GenBank/DDBJ.databases.
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Best Local :
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01-MAY-2000
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MEDLINE=20530913; pubMed=11076861; DOI=10.1101/gr.152600;

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watchiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

"RIKEN integrated sequence analysis (RISA) system=384-format

sequencing pipeline with 384 multicapillary sequencer.";

Genome Res. 10:1757-1771(2000).
                                                                                  SEQUENCE FROM N.A. MEDLINE=99316314; PubMed=10384126; Ribas G., Neville M., Wixon J.L.,
                                                                                                                                                                                                                                   Homo sapiens (Human)
Eukaryota; Metazoa; (
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                       GGe protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9UMP8;
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   Ribas G., Neville M., Wixon J.L., Cheng J., Campbell R.D.; "Genes encoding three new members of the leukocyte antigen 6 "Genes encoding three newher of Ig superfamily, together with genes superfamily and a novel member of Ig superfamily. Together with genes encoding the regulatory nuclear chloride ion channel protein (hRNCC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
encoding
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Primates;
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Last annotation update)
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Catarrhini;
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i; Hominidae; Homo.
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Hori F.,
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STRAIN=C57BL/GJ; TISSUB-Stomach; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibatea Y., Hayatsu N., Sugahara Y., Shibata Konno H., Okazaki Y., Muramatsu M., Hayatshizaki Y.; "Normalization and subtraction of cap-trapper-selected cD prepare full-length cDNa libraries for rapid discovery of Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE-Stomach;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM Consortium;
"Functional annotation of a full-length mouse cDNA colle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6J; TISSUE=Stomach; MEDLINE=99279253; PubMed=10349636; Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA C Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Last sequence 01-MAR-2004 (TrEMBLrel. 26, Last annotati Mus musculus adult male stomach cDNA, RIF Library, clone:2210003103 product:weakly ASSOCIATED GPI-ANCHORED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9D7Z7;
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Genomics 80:113-123(2002).
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                                                                                                                                                                                                                                                the RIKEN Genome Exploration Research Group "Analysis of the mouse transcriptome based 60,770 full-length CDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=2210003I03Rik;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                         The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
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                                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/6J; TISSUE=Stomach;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                            SEQUENCE FROM
                                                                                                                                                                                                                           Vature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             v
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AJ245419; CAB52193.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
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                                                                                                                                                                                                                              420:563-573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -GKSCLSRAQCPLPGYATYWLHSYTLWHHCCEQDLCNIAASPQQL---TSLLASLPLFV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INKGCLRATSCGLEEPVSYRGVTYSLTTNCCTGRLCNRAPSSQTVGATTSLALGLGMLL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LFLCGALGLTMS---PARGRLRCYICGFT--KPCHPVPTECRDDEAC----GISIGTS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125 AA;
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13524 MW;
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Last annotation update)
mach cDNA, RIKEN full-length enriche
roduct:weakly similar to METASTASIS-
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P SEQUENCE FROM N.A.

C STRAIN=C57BL/6J; TISSUE=Stomach;

C MBDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

W MBDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

W MBDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

W MBDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

W MBDLINE=20530913; PubMed=110.76861; DOI=10.1101/gr.152600;

W MBDLINE=20530913; PubMed=110.76861; DOI=10.1101/gr.152600;

W ABGULINE=20530913; PubMed=110.76861; N. Nagaaka S., Kasaki T., Harada A., Watanira S., Kashiwagi K., RA Yunenda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Watanira S., Watanira S., Kawai J., Watanira S., Watanira S., Kawai J., Watanira S., Watanira S., Kawai J., Watanira S., Kawai J., Watanira S., Kawai J., Watanira S., Watanira S., Watanira S., Kawai J., Watanira S., Watanir
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RA Adachi J., Alzawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carminci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Arakawa T., Bono H., Carminci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiracka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Kawai Y., Okido T., Owa C., Saito H., Saito R., Sakai K.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Godabe Y., Suzuki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sama Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.,
RA Muramatsu M., Hayashizaki Y.,
Shi KMAT, MKO08654, BABZS810.1; -.
DR KMEL; AKO08654, BABZS810.1; -.
DR KMEL; AKO08654, BABZS810.1; -.
DR MGD; MGI:1924192; 2210003I03Rik.
DR InterPro; IPR001526; LY6 UPAR.
DR SMART; SM00134, LUJ. 1.
DR PROSITE; PS00993; LY6 UPAR; UNKNOWN 1.
SEQUENCE 256 AA; 27450 MW; D66B55762C8D767B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q6MG57;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Lymphocyte antigen 6 complex, locus G6E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=Ly6g6e;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q6MG57
                                                             STRAIN-Brown Norway;
PubMed=15060004; DOI=10.1101/gr.1987704;
Hurt P. Walter L., Sudbrak R., Klages S., Mu
Inoko H., Lehrach H., Guenther E., Reinhardt
                                                                                                                                                                                                                                                                                                                                                       Mammalia;
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
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ota; Metazoa; Chordata;
ia; Eutheria; Rodentia;
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                                comparative
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Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
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                            s S., Mueller I.,
inhardt R., Himmel
analysis of the 1
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J. 042;
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Himmelbauer H.;
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RESULT RESULT AC SERVICE RESULT RESUL
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                                                                                                                                                 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Schriml L.M., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Baldarelli R., Hill D.P., Bult C., Gotorbani L.E., Cousins S.,
RA Balke J.A., Eract D., Brusic V., Cotothia C., Corbani L.E., Cousins S.,
RA Balke J.A., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Balke J.A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Gassterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Gasterland T., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Magashina T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Secou M., Shinada K.,
RA Verardo R., Wanhaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Vuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Komno H., Nakamura M., Sakazume N., Sato K.,
RA Hirozane-Kishikawa T., Komio H., Nakamura M., Sakazume N., Sato K.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Hara A., Hayashizaki Y.,
RA Hara A., Hayashizaki Y.,
RA Hara A., Hayashizaki Y.,
RA Hara B., Hayashizaki Y.,
RA Har
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Boehm S., Borzym K., Gelling S., Gimmel V., Heitmann K., Kosiur
Lang N., Lehrack S., Thiel J., Sontag M., Hurt P., Himmelbauer
Sudbrak R., Reinhardt R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; EX883045; CAE8399.1; - CANDORFO77FF4CB4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C57BL/6J; TISSUE=Eye; MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=C57BL/6J; T
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25-JAN-2005 (Rel. 46, Last sequence up
25-JAN-2005 (Rel. 46, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein EPGP3023 precursor.
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Genome Res. 14:631-639(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria;
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RA Klausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Butog. K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Scheutz J., Myers R.M.,
RA Buteerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.",
RT "Groc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC --- SUBCELULAR LOCATION: Secreted (By similarity).
CC --- SUBCELULAR LOCATION: Secreted (By similarity).
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CARBOHYD
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SIGNAL
                               Insulin-like growth
Name=IGFBP6;
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Homo sapiens (Human)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
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                                                                                                                                                                                                                                                                                          DIY--CPRDTRYCYTQHTMEVTGNSISVTKRCVPLEECLSTGCRDS-EHEG--YKICTSC
                                                                                                                                                                                                                                                                                                                          GTYMHC-GDDEDCFTGHGV-APGTGPVINKGCLRATSC---
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                                                                                                                                                                                                                                                         CTGRLCN-RAPSSQT--VGATTS 110
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(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
growth factor binding protein 6 (Fragment).
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15; Mismatches 4
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Protein EPGP3023.
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N-linked (GlcNAc. . .) (Potential).
N-linked (GlcNAc. . .) (Potential).
1 N-linked (GlcNAc. . .) (Potential).
2 AF886868BDE5CC4 CRC64;
 Craniata; Vertebrata; Euteleostomi;
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1BB6 HUMAN STANDARD; PKT; 240 Am.
194592; Q14492;
01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
1nsulin-like growth factor binding protein 6;
6) (IGF-binding protein 6).
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=21167382; PubMed=11267670; DOI=10.1016/S0167-4781(01)00192-0; Dailly Y.P., Zhou Y., Linkhart T.A., Baylink D.J., Strong D.D.;

"Structure and characterization of the human insulin-like growth factor binding protein (IGFBP)-6 promoter: identification of a functional retinoid response element.";

Functional retinoid response element.";
                           SEQUENCE
Rieder M.
                                                                                                                                                                                                                                                                                                                   MEDLINE=91225006; PubMed=1709161; Kiefer M.C., Masiarz F.R., Bauer D.M., Zapf J.; Tidentification and molecular cloning of two new 30-kDa insulin-like growth factor binding proteins isolated from adult human serum."; J. Biol. Chem. 266:9043-9049(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP;
GO; G
                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=99189142; PubMed=10087296;
Ehrenborg E., Zazzi H., Lagercrant.
Allander S.V., Larsson C., Luthman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                               Ehrenborg E., Zazzi H., Lagercrantz S., Granqvi Allander S.V., Larsson C., Luthman H.; Allander s. V., Larsson C., Luthman H.; "Characterization and chromosomal localization like growth factor-binding protein 6 gene."; Wanm. Genome 10:376-380(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Osteosarcoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005520; F:insulin-like growth factor
GO; GO:0001558; P:regulation of cell growth;
InterPro; IPR009030; Grow_fac_recept.
InterPro; IPR009867; Insl_gro_fac_pr.
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NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=IGFBP6; Synonyms=IBP6;
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  I.J., L
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  FROM N.A., AND .J., Livingston K.E., Nguyen C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ŗ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.3%;
VARIANTS GLY-128 AND GLN-217.
R.J., Daniels M.R., Chung M.-W.
.P., Nguyen D.A., Poel C.L., Rob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
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Pred. No. 0.041;
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Robertson

P.D.,

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collaboration outstation

acetylhexosamine (probably GalNAc) and sialic acid residues. Major glycoforms consist of 8-16 monosaccharides (by homology to IGPBP-6 expressed recominantly in CHO cells).

-i- SIMILARITY: Contains 1 IGFBP domain.

-i- SIMILARITY: Contains 1 thyroglobulin type-I domain.

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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., WcEwan R.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Rahes J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shewchenko Y., Bouffard G.G.,

RA Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Isolation and protein-6.";
Mol. Endocrinol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98241382; PubMed=9572875; DOI=10.1021/bi972894e;
Neumann G.M., Marinaro J.A., Bach L.A.;
"Identification of O-glycosylation sites and partial characterization
of carbohydrate structure and disulfide linkages of human insulin-like
growth factor binding protein 6.";
Biochemistry 37:6572-6585(1998).
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                                                                                                                                                                                                                                                                                                                                                                             determined by mass spectrometry.";
J. Biol. Chem. 274:14587-14594(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neumann G.M., Bach L.A.;
"The N-terminal disulfide linkages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Cerebrospinal fluid;

MEDLINE=90005986; PubMed=2551732; DOI=10.1016/0014-5793(89)81101-9;

Roghani M., Hossenlopp P., Lepage P., Balland A., Binoux M.;

Roghani m. Hossenlopp P., Lepage P., Balland A., Binoux M.;

"Isolation from human cerebrospinal fluid of a new insulin-like grove factor binding protein with a selective affinity for IGF-II.";

FEBS Lett. 255:253-258(1989).
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MEDLINE=92049376; PubMed=1719383;
MEDLINE=92049376; PubMed=1719883;
MEDLINE=92049376; PubMed=1719883;
MEDLINE=92049376; PubMed=1719883;
MEDLINE=9204938;
MEDLINE=920493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            factor-binding protein-6 (hIGFBP-6) and hIGFBP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99262603; PubMed=10329650; DOI=10.1074/jbc.274.21.14587;
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MEDLINE=91207395;
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TISSUE-Cerebrospinal fluid;
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                                                    FUNCTION: IGF-binding proteins prolong the half-life of the IGFs and have been shown to either inhibit or stimulate the growth promoting effects of the IGFs on cell culture. They alter the interaction of IGFs with their cell surface receptors.

SUBCELLULAR LOCATION: Secreted.
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glycans consist
of hexose (probably Gal),
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insulin-like growth factor-binding
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EMBL; AY443494; AAR05445.1; --
EMBL; BC003507; AAH03507.1; --
EMBL; BC005007; AAH0507.1; --
EMBL; BC010162; AAH10162.1; --
EMBL; BC011708; AAH11708.1; --
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Pfam; PF00086; Thyroglobulin 1; 1.

PIRSF; PIRSF001969; IGFBP1-6; 1.

SMART; SM00121; IB; 1.

SMART; SM00211; TY; 1.
                                                                                                                                                                                                                                                                                                                                                                       InterPro; InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                        PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cullies requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
                                                                                    VARIANT
                                                                                                                                                                                                                                                                                       PROSITE; PS00222; IGF BINDING; raus PROSITE; PS00484; THYROGLOBULIN 1;
                                                                                                                                                                                                                                                                                                                                                                                                                HSSP;
                                                                   CONFLICT
                                                                                                     VARIANT
                                                                                                                                               CARBOHYD
                                                                                                                                                        CARBOHYD
                                                                                                                                                                                DISULFID
                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                    MIM; 146735; -.
GO; GO:0008285; P:negative regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M62402; AAB06187.1; -.
                                                                                                                      VARIANT
                                                                                                                                                                                                                                                                                   Direct protein sequencing; Glycoprotein; Growth
                                                                                                                                                                                                                                                                                                                                                                                                        Genew; HGNC:5475; IGFBP6.
                                                                                                                                                                                                                                                                           Polymorphism;
                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                        A39842; A39842.
S05699; S05699.
                                                                                                                                                                                                                                                                                                                                                                                                                                         M69054; AAA88070.1;
                                  Similarity
LCWLLLLVMALPPGTTGVKDCVFCELTDSMQCPGTYMHCGDDEDCFTGHGVAPGTGPVIN
                                                                                                                                                                                                                                                                                                                                                    IPR009030; Grow fac recept.
IPR009168; IGFBP1-6.
IPR000867; Insl_gro fac pr.
IPR000716; Thyroglobulin_1.
                                                          240
                          Conservative
                                                                                                                                                               78
163
201
214
126
                                                                                                                                                                                                                                                                           Signal
                                                                                                                                                                                                                                                                                                                                                                                                                 1BOE
                                                           A
                                                                                                                                                                                                                                                                                                    IGF_BINDING; FALSE_NEG
                                                                                                                     234
32
63
63
104
104
1190
212
212
212
234
144
144
144
144
126
144
128
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240
                                                           2
25322
                                 15.3%;
                                                           W.
                          10;
                                                                                                                             O-linked
O-linked
O-linked
O-linked
O-linked
                         Score 104.5; DB
Pred. No. 0.084;
0; Mismatches
                                                                                    /FTId=VAR_018933.
T -> P (in dbsNP:1053134).
                                                                                                                                                                                                                                        Insulin-like growth factor binding protein 6.
Thyroglobulin type-I.
                                                                           T -> P (in dbSNP
/FTId=VAR_011907
                                                                                                                                                                                                                                                                     Probable
                                                                                                          /FTId=VAR_018932
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                                        DB 1;
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                          50;
                                                                                                                                                                                                                                                                                                                                                                                        proliferation; TAS
                                                                                                                                                                                                                                                                                     factor binding;
                                                             CRC64;
                                          Length
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y similarity).
y similarity).
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                           Gaps
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Q9D7E5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
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Q9D7E5;
Q9D7E5;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Mus musculus adult male tongue cDNA, RIKEN full-length enriched
library, clone:2310011102 product:putative Ly-6 superfamily member,
full insert sequence (Ly6g6e protein, isoform A).
                                                                              STRAIN=C57BL/6J; TISSUE=Tongue;

MEDLINB=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RIKEN integrated sequence analysis (RISA) system-384-format

pequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

STRAIN-C57BL/6J; TISSUE=Tongue;

MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;

Carninci P., Shibata Y., Hayatfu N., Sugahara Y., Shibata K., Itoh M.,

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prepare full-length cDNA libraries for rapid discovery of new genes.";

Genome Res. 10:1617-1630(2000).
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STRAIN-C57BL/6J; TISSUE-Tongue;
MEDLINE-99279253, PubMed-10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Tongue;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM Consortium;
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation 60,770 full-length cDNAs."; Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Tongue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690\,(2001).
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----NCAPGLQCH--PPKDDEAPLRALLLGRGRCLP 106
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Best Local S
Matches 31
                                                                                                                                                                                          PROUBNICE FROM N.A., AND SEQUENCE OF 21-33.

MEDLINE-95310346; PubMed=7790363; DOI=10.1083/jcb.129.6.1677; Brakenhoff R.H., Gerretsen M. Knippels E.M.C., van Dijk M., van Essen H., Weghuis D.O., Sinke R.J., Snow G.B., van Dongen G.A.M.S.;

"The human E48 antigen, highly homologous to the manual ThB, is a GPT-section."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
Katai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T.,
Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
Muramatsu M., Hayashizaki Y.,
SEQUENCE FROM N.A.
MEDLINE=98031741; PubMed=9366413;
Brakenhoff R.H., van Dijk M., Rood-Knippels.E.M.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q14210; Q43783; Q8TBD4; Q92933;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Lymphocyte antigen Ly-6D precursor (E48 ant
Name=LY6D; Synonyms=E48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AX009303; BABZ6204.1; -.
EMBL; AJ31550; CAC85546.1; -.
EMBL; MGJ1917524; Ly6g6e.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005024; F:transforming growth factor beta receptor ac.
InterPro; IPR000472; Activin receptor.
InterPro; IPR001526; LY6_UPAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIINE-22074936; PubMed=12079290; DOI=10.1006/geno.2002.6794; Mallya M., Campbell R.D., Aguado B.; "Transcriptional analysis of a novel cluster of LY-6 family members in the human and mouse major histocompatibility complex: five genes with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        many splice forms.";
Genomics 80:113-123(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6J; TISSUE=Tongue;
                                                                                                                                                                                                                                                                                                                                                                                                                                 CBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAMUH [D9X]
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                                                                                                                              . Cell Biol.
                                                                                                                                                          is a GPI-anchored molecule apparently
.-cell adhesion.";
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7; SM00134; LU; 1.
2NCE 134 AA; 14600 MW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTTGVKD-----CVFCELTDSMQCPGTYMHCGDDEDCFTGHGVAPGTGP-----VI
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                                                                                                                              129:1677-1689(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.2%;
                                                                                                                                                                                       highly homologous to the murine Ly-6 antigen molecule apparently involved in keratinocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7;
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Pred. No. 0
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(E48 antigen).
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., AR Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., A Brownstein M.J., Wollano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Maka S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H., A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Vallalon D.K., Morley R.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Vallalon D.K., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., A Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., A Rahring M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Blakesley R.W., Touchman J.W., Scheintz J., Myers R.M., Schein J.E., Jones S.J.M., Warra M.A.;

"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
                                                                             GO; GO:0005624; C:membrane fraction; TX
GO; GO:0007155; P:cell adhesion; TAS.
InterPro; IPR003632; Ly-6 CD59.
InterPro; IPR001526; LY6 UPAR.
Pfam; PF00021; UPAR. LY6; 1.
SMART; SM00134; LU; 1.
PROSITE; PS00983; LY6 UPAR; 1.
PROSITE; PS00983; LY6 UPAR; 1.
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verified c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercia entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
Lipoprotein; Membrane; Multigene family; Signal.
SIGNAL 1 20
CHAIN 21 98 Lymphoryte ---
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                                                                                                                                                                                                                                                                                          H-InvDB; HIX0007832; -.
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Genew; HGNC:13348; LY6D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              verified cleavage sites.";
Protein Sci. 13:2819-2824(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=15340161; DOI=10.1110/ps.04682504; Zhang Z., Henzel W.J.;
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SIMILARITY: Contains 1 UPAR/Ly6 domain.
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RESULT 12
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ID Q9NZJ
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AC Q9NZJ
O1-OC
DT 01-OC
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DT Megak
GN Name
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OC Eukaz
OC Mamma
OX NCB1
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Matches 36
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InterPro; IPR003599; IG.
InterPro; IPR007110; Ig-like.
SMART; SM00409; IG; 1.
PROSITE; PS50835; IG LIKE; 1.
PROSITE; PS50835; IG LIKE; 1.
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Q9NZJ1;
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01-OCT-2000
01-OCT-2003
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Submitted (OCT-1999) to the
EMBL; AF195764; AAF35181.1;
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                WILMLLITMGQGVVILALSIVLWRQRVRGAPGRGNRMRCYNCGGSPSSSCKEAVTTCGEG
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NSAVASHVAPAGILAAAATALTCLLP
                                    NRAPSSOT -- VGATTSLALGLGMLLP
                                                                                R---PQPGLEQIKLPGNPPVTLIHQHPACVAAHHCNQVETESVGDV
                                                                                                                      EDCFTGHGV----APGTGPVI----NKGCLRATSCGLEEPVSYRGVTYSLTTNCCTGRLC 96
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25.3%; Pred. No. 0.2;
cive 13; Mismatches
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By similarity.
CPI anchor amidated and (Potential).
A - T (in Ref. 2).
K -> E (in Ref. 4).
C -> L (in Ref. 4).
C -> L (in Ref. 4).
C -> C C -> CR
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Pred. No. 0.0
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RESULT 13

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RP SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

RC STRAIN=TBJN; TISSUB=Salivary gland;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.24260389;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426036;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603(2002).

RX MEDLINE=22388257; PubMed=12477932
MGD; MGI:96881; Ly6d.
InterPro; IPR003632; Ly-6 CD59.
InterPro; IPR001526; LY6 UPAR.
Pfam; PF00021; UPAR LY6; 1.
ProDom; PD003128; Ly-6 CD59; 1.
SMART; SM00134; LU; 1.
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01-JUN-1994
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05-JUL-2004 (Rel. 44, Last annotation update)
Lymphocyte antigen Ly-6D precursor (Thymocyte
Name=Ly66; Synonyms=Ly61, Thb;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertel
Mammalia; Eutheria; Rodentia; Sciurognathi; M
                                                                                                                                                              EMBL; X63782; CAA45317.1; -.
EMBL; L40419; AAA79249.1; ALT_INIT.
EMBL; BC025135; AAH25135.1; -.
                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restrues by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-s or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gumley T.P., McKenzie I.F., Sandrin M.S.; "Sequence and structure of the mouse ThB Immunogenetics 42:221-224(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE-Thymocyte8;
MEDLINE-33017863; PubMed-1401899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=BALB/c; TISSUE=Leukocyte; MEDLINE=95369850; PubMed=7642235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gumley T.P., McKenzie I.F., Kozak C.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Isolation and characterization of B cell antigen (ThB).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TX6D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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RESULT 14
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Best Local
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               Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Wilting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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25-JAN-2005 (Rel.
25-JAN-2005 (Rel.
Protein EPGP3023 I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The secreted protein discovery initiative (SPDI), effort to identify novel human secreted and transme bioinformatics assessment."; Genome Res. 13:2265-2270(2003).
                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yi S., Yu G., Yuan J., Zhang
Godowski P., Gray A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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RESULT 15
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Best Local S
Matches 43
SEQUENCE FROM N.A.
TISSUB-AORTIC endothelium;
TISSUB-BOITIC endothelium;
MEDLINE-98217182; PubMed-9558099;
Hinchliffe S.J., Rushmere N.K., Hanna S.M., Morgan
Hinchliffe S.J., Rushmere N.K., Hanna S.M., Morgan
"Molecular cloning and functional characterization
of CD59: relevance to xenotransplantation.";
of CD59: relevance to xenotransplantation.";
                                                                                                                                                                                                                062680; Q9TR76; Q9XT94;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
CD59 glycoprotein precursor (Membrane attack complex inhibition factor) (MAC-IP) (MAC-inhibitory protein) (MAC-IP) (Protectin).
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CARBOHYD
                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                           NCBI_TaxID=9823;
                                                                                                                                                                                         Sus scrofa (Pig).
                                                                                                                                                                                                           Name=CD59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct protein sequencing; Signal. SIGNAL 1 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhang Z., Henzel W.J.;
"Signal peptide prediction based on analysis
verified cleavage sites.";
Protein Sci. 13:2819-2824(2004).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                    CD59 PIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=15340161; DOI=10.1110/ps.04682504; Zhang Z., Henzel W.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Secreted. SIMILARITY: Contains 1 UPAR/Ly6 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
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171 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 99; DB
Pred. No. 0.2;
Pred. No. 0.2;
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w-linked (GlcNAc. . .) (Potential).
n-linked (GlcNAc. . .) (Potential).
n-linked (GlcNAc. . .) (Potential).
; lbAEEE9CD18F5470 CRC64;
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                                                                                                                                                                            RC TISSUE=Erythrocyte;

RX MEDLINE=59181826; PubMed=7533195; DOI=10.1016/0022-1759(94)00288-8;

RX wan den Berg C.W., Harrison R.A., Morgan B.P.;

RA van den Berg C.W., Harrison R.A., Morgan B.P.;

RT wanden Berg C.W., Harrison R.A., Morgan B.P.;

RT "A rapid method for the isolation of analogues of human CD59 by

RT preparative SDS-PAGE: application to pig CD59.";

RI J. Immunol. Methods 179:223-231(1995).

CC complex (MAC) action. Acts by binding to the C8 and/or C9

CC complex (MAC) action. Acts by binding to the C8 and/or C9

CC complements of the assembling MAC, thereby preventing

CC incorporation of the munitiple copies of C9 required for complete

CC formation of the osmolytic pore.

C1- SUBCELIULAR LOCATION: Attached to the membrane by a GPI-anchor.

CC 1. TISSUE SPECIFICITY: Expressed in all tissues tested (lung, testis

CC in lung and spleen, heart and skeletal muscle). Highest levels

CC in Ilung and spleen, lowest levels in liver and skeletal muscle.

CC -:- SIMILARITY: Contains 1 UPAR/Ly6 domain.
                                                                                   Query Match
Best Local S
Matches 33
                                                                                                                                                                       CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                  DOMAIN
DISULFID
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                                                                                                                                                                                                                                                              LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProDom; PD003128; LU; SMART; SM00134; LU;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003632; Ly-6 CD59
InterPro; IPR001526; LY6 UPAR.
Pfam; PF000021; UPAR LY6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF020302; AAC67231.1; -.
EMBL; AF058328; AAD39837.1; -.
HSSP; P13907; LERG.
InterPro; IPR003632; Ly-6_CD59.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
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SEQUENCE OF 26-123 FROM
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                                                                                                            Similarity
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                                             VLCWLLLLVMALPPGTTGVKDCVFCELTDSMQC-----PG----TYMHCGDDED-CFTGH
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                                                                                      Conservative
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                                                                                                                                                                   LY6_UPAR; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          characterization of porcine CD59:
                                                                                                        14.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequencing; Glycoprotein;
                                                                                      15;
                                                                                                                                                                                          Removed in mature for UPAR/Ly6.

By similarity.
By 
                                                                                 Score 98.5; DB 1; Pred. No. 0.16; 5; Mismatches 47.
  -- AVLCHLGHSLQCYNCINPAGSCTTAMNCSHNQDACIFVE
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52

GVAPGTGPVINKGCLRATSCGLEEPVSYRGVTYSLTTNCCTGRLCNRAPSSQTVGATTSL

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Db 56 AVPPKT----YQCWRFDECNFDF-ISRNLAEKKLKYNCCRKDLCNKSDATISSGKTALL 110

QY 112 AL 113

Db 111 vi 112

Search completed: April 15, 2005, 14:04:11

Job time: 193 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 15, 2005, 14:00:50; Search time 16 Seconds (without alignments) 745.680 Million cell updates/sec

Title:
Perfect score:
Sequence: US-10-809-654-16
684
1 MVLCWILLLIAMALPPGTTGV......VGATTSLALGLGMLLPPRLL 124

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	29	28	27	26,	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	æ	7	6	5	4	ω	2	<b>,</b>	No.	Result	
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	activin A receptor	neurotoxin homolog	short neurotoxin 4	hypothetical prote	surface glycoprote		ъ	prespore vesicle p	activin receptor-l	hypothetical prote	short neurotoxin 3	Delta-4 protein -	activin receptor I	transforming growt					urokinase-type pla		urokinase-type pla	urokinase-type pla	alpha-2-macroglobu		hypothetical prote	gene ThB protein -	phosphatidylinosit	E48 antigen precur	g.	; 'g		

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1321	153	249 496	1252	603	134	82	161	158	81	509	248	136	122
2 1	N	NN	N	N	N	N	N	N	N	N	N	N	N
A29941 JE0352	A34132	T31837 T41114	S36016	S28941	A25708	JC5892	A46189	B34132	S27366	A49664	T31841	I49013	PN0622
t-plasminogen acti mucin MUC5B, trach	vasotocin / neurop	hypothetical prote uroporphyrin methy	oocyst wall protei	coagulation factor	Ly-6.1 protein pre	cobrotoxin b - Chi	vasotocin - Pacifi	vasotocin / neurop	metallothionein E(	activin type I rec	hypothetical prote	thymic shared anti	insulin-like growt

## ALIGNMENTS

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C;Superfamily: Ly-6 antigen; Ly-6 homology C;Keywords: blocked carboxyl end; cell adhesion; glycoprotein; lipoprote F;1-20/Domain: signal sequence #status predicted <SIG> F;21-100/Domain: Ly-6 homology <LY6> F;21-100/Domain: Ly-6 homology <LY6> F;21-93/Product: B48 antigen #status predicted <MAT> F;23-945,26-32,38-63,67-86,87-92/Disulfide bonds: #status predicted F;23-45,26-32,38-63,67-86,87-92/Disulfide bonds: #status predicted (Asn)
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C;Accession: A57321
R;Brakenhoff, R.H.; Gerretsen, M.; Knippels, E.M.C.; van Dijk, M.; van Essen, H.;
J. Cell Biol. 129, 1677-1689, 1995
A;Title: The human E48 antigen, highly homologous to the murine Ly-6 antigen ThB,
A;Reference number: A57321; MUID:95310346; PMID:7790363
A;Accession: A57321
  phosphatidylinositol-anchored B-cell N;Alternate names: thymocyte B-cell a
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                                        A46528
                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:Q14210; GB:X82693; NID:g887453; PIDN:CAA58014.1; PID:g887454
A;Note: parts of this sequence, including the amino end of the mature protein, were conf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-128 < BRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Date: 08-Dec-1995 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-240/Product: insulin-like growth factor-binding protein 6 #status predicted F;163-234/Domain: thyroglobulin type I repeat homology <THYI>
F;229/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Superfamily: insulin-like growth factor binding protein; thyroglobulin type I repeat C;Keywords: glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Map position: 8q24-qter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Genetics:
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Best Local Similarity
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                                                                                                                                                                                                                                 66 LRATSCGLEEPVSYRGVTYSLTTNCCTGRLCN----RAPSSQTVGATTSLALGLGM----
                                                                                                                                                                                                                                                                                                                                                  36;
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                                                                                                                                                                                                                                                                                                              6 LLLLVMALPPGTTGVKDCVFCELTDSMQCPGTYMHCGDDEDCFTGHGVAPGTGPVINKGC
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                                                                                                                      VILAPSL 128
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%; Pred. No. 0.032;
10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                        Score 102.5; DB Pred. No. 0.029;
antigen
                      antigen
                                                                                                                                                                                                                                                                            -TSSSNCKHSVVCPASSRFCKTTNTVEPLRGNLVKKDC
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ThB
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<SIG>
                    precursor -
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C;Species: Mus musculus (nouse mouse, C;Date: 18-Jun-1993 #sequence_revision 16-Aug-1996 #text_ch C;Date: 18-Jun-1993 #sequence_revision 16-Aug-1996 #text_ch C;Accession: A46528 R;Gunley, T.P.; McKenzie, I.F.; Kozak, C.A.; Sandrin, M.S. J. Immunol. 149, 2615-2618, 1992 A;Title: Isolation and characterization of cDNA clones for A;Reference number: A46528; MUID:93017863; PMID:1401899 A;Accession: A46528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene ThB protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 23-Jul-1999
C;Accession: I54553
R;Gumley, T.P.; McKenzie, I.F.; Sandrin, M.S.
Immunogenetics 42, 221-224, 1995
A;Title: Sequence and structure of the mouse ThB gene.
A;Title: Sequence and structure of the mouse ThB gene.
A;Reference number: I54553; MUID:95369850; PMID:7642235
A;Accession: I54553
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-127 GGUM>
A; Cross-references: UNIPROT: p35459; GB: X63782; GB: S46666; NID: g288264; PIDN: CAA45317.1; I
A; Cross-references: UNIPROT: p35459; GB: X63782; GB: S46666; NID: g288264; PIDN: CAA45317.1; I
A; Experimental source: C57BL/6; ppleen cells, thymocytes
A; Note: sequence extracted from NCBI backbone (NCBIP: 116104)
C; Comment: This 15K GPI-anchored surface antigen is found on B thymocytes and B cells.
C; Genetics:
A; Gene: Thib
A; Map position: 15
C; Superfamily: Ly-6 antigen; Ly-6 homology
C; Keywords: blocked carboxyl end; glycoprotein; lipoprotein; phosphatidylinositol linkage
F; 1-20/Domain: signal sequence #status predicted <STG>
F; 21-100/Domain: Ly-6 homology <LYCs-
F; 21-100/Domain: Carboxyl-terminal propaghtide #status predicted <CTP>
F; 93/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Asn) (in mature form)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated
A;Molecule type: DNA
A;Residues: 1-130 <RES>
                                                                                                                                                                                                                                                                                                                                                                            A; Introns: 21/1; 54/1
C; Superfamily: Ly-6 antigen; Ly-6 homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:L40419; NID:g1019624; PIDN:AAA79249.1;
                                                                                                                                                                                                                                Query Match
Best Local S
Matches 37
                                                                                                                                                                                                                                                                                                                                                ;24-103/Domain: Ly-6 homology
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Best Local (
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Date: 18-Jun-1993 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                             LILLYMALPPGTTGVKDCVFCELTDSMOCPGTYMHCGDDEDCFTGHGVAPGTGPVINKGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVLLVLAVATSPAWALRCHVC--TNSANCKNPQVCPSNFYFCKTVTSVEPLNGNLVRKEC 63
--ANSCTSDYSQQGHVSSGSEVTQCCQTDLCNERLVSAAPGHALLSSVTLGLATSLSL
                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                14.8%; Score 101; DB 2
31.4%; Pred. No. 0.039;
rative 12; Mismatches
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                                                      AP----SSQTVGATTSLAL 113
                                                                                                                                                                                                                                                                                          Length 130;
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A; Map position: 1
A; Introns: 26/1; 51/1; 195/1
A; Introns: 26/1; 51/1; 195/1
C: Superfamily: Caenorhabditis elegans hypothetical protein F48G7.8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Miller, N.; Bradshaw, H.; Wamsley, P.
submitted to the EMBL Data Library, February 1997
A;Description: The sequence of C. elegans cosmid C46Hll
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein C46H11.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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"השפריוחtion: The sequence of C. elegans cosmid T10E10.
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A;Experimental source: strain Bristol N2; clone C46H11
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A;Residues: 1-1101 <GEI>
A;Cross-references: UNIPROT:Q22378;
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
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Best Local :
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nB: 93/2; 152/2; 191/3; 209/2; 283/3; 303/1; 399/3; 421/1; 440/1;
                                                                  153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                  TARASLCN-
                                                                                                             CLRATSCGLEEPVSYRGVTYSLTTNCCTGRLCNRAPSSQTVGATTS 110
                                                                                                                                                        STGVSDCPALAYLCNDTTTYYTVMTQQCPRTCGRCNSTTTSSTSCADLVNPSTG--VSDC 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGTSQCQNKVCCQQTDTLNLNNLIQHQAPLCPGSNVPPLGSC--NEQCPQYSACTPGLGC 449
                                                                                                                                                                                                     TTGVKDC----VFCELTD-----SMQCPGTYMHCGDDEDCFTGHG--VAPGTGPVINKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IVYNVVLLCPDGTPSTTSCSKGCG 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TV-----GATTSLALGLG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CPVPVNEQPTGMIKITLC----PGSY-SPPFGVCGSCPSGTQCNQQLQMCCPLQQQPSTD 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -PV-INK---GCLRATSCGLEEPVSYRGVTYSLTTNCCTGRLCN-----RAPSSQ 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGTTGVKDCVFCELTDSMQ------CPGTYM----HCGDDEDCFTGHGVAPGTG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                              12.3%; Score 84; DB 2; Length 240; 30.2%; Pred. No. 2.1; cive 10; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.5%; Score 85.5; DB 2; Length 1101; 25.7%; Pred. No. 5.7;
                                                                  -DSVYYAVMTQQCP-RTCGRCNSSSTVTSSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bristol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21;
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51 N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                  190
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                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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F;117-150/Domain: EGF homology <EG1>
F;126-190/Domain: EGF homology <EG2>
F;200-241/Domain: LDL receptor YWTD-containing rep F;242-283/Domain: LDL receptor YWTD-containing rep F;242-283/Domain: LDL receptor YWTD-containing rep F;242-283/Domain: LDL receptor YWTD-containing rep F;337-380/Domain: LDL receptor YWTD-containing rep F;337-380/Domain: LDL receptor YWTD-containing rep F;423-470/Domain: LDL receptor YWTD-containing rep F;423-470/Domain: LDL receptor YWTD-containing rep F;616-661/Domain: LDL receptor YWTD-containing rep F;616-661/Domain: LDL receptor YWTD-containing rep F;617-3754/Domain: LDL receptor YWTD-containing rep F;713-754/Domain: LDL receptor YWTD-containing rep F;155-797/Domain: LDL receptor YWTD-containing rep F;155-840/Domain: LDL receptor YWTD-containing rep F;852-888/Domain: LDL receptor ligand-binding repe F;934-959/Domain: LDL receptor ligand-binding repe F;934-959/Domain: LDL receptor ligand-binding reperiors.
                                                                                                                                                                                                                                                F;1930-1972/Domain:
F;1973-2015/Domain:
F;2016-2059/Domain:
F;2060-2101/Domain:
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A; Residues: 1-4543 «NIM»
A; Residues: 1-4543 «NIM»
A; Residues: 1-4543 «NIM»
C; Complex: The alpha-2-macroglobulin receptor complex consists of noncovalently-associate
C; Complex: The alpha-2-macroglobulin receptor; EGF homology; LDL receptor ligand-binding
C; Superfamily: alpha-2-macroglobulin receptor; EGF homology; LDL receptor ligand-binding
C; Keywords: beta-hydroxyasparagine; beta-hydroxyaspartic acid; calcium binding; glycoprot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alpha-2-macroglobulin receptor precursor - chicken
N;Alternate names: CD91; LDL receptor-related protein 1; low density lipoprotein
C;Species: Gallus gallus (chicken)
C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 09-Jul-2004
C;Accession: A53102
R;Nimpf, J.; Stifani, S.; Bilous, P.T.; Schneider, W.J.
J. Biol. Chem. 269, 212-219, 1994
                                                                                                                            F;2102-2147/Domain:
F;2155-2190/Domain:
F;2195-2237/Domain:
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            F;2247-2288/Domain:
F;2338-2382/Domain:
F;2383-2423/Domain:
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in: LDL receptor ligand-binding repeat homology <LDLA>
in: LDL receptor ligand-binding repeat homology <LDLB>
in: LDL receptor YMTD-containing repeat homology <W112>
in: LDL receptor YMTD-containing repeat homology <W113>
in: LDL receptor YMTD-containing repeat homology <W21>
in: LDL receptor YMTD-containing repeat homology <W21>
in: LDL receptor YMTD-containing repeat homology <W22>
in: LDL receptor YMTD-containing repeat homology <W23>
in: LDL receptor YMTD-containing repeat homology <W27>

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receptor ligand-binding repeat homology <LDL3>
receptor ligand-binding repeat homology <LDL4>
receptor ligand-binding repeat homology <LDL5>
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Y <YW02>
Y <YW03>
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F;4421-4443/Domain: transmembrane #status predicted <INT>
F;4421-4443/Domain: intracellular #status predicted <INT>
F;4444-453/Domain: intracellular #status predicted <INT>
F;116,138,187,276,359,448,731,926,1048,1152,1153,1193,1216,1305,1509,1556,1573,1614,1643
3485,3659,3786,3837,3952,4074,4124,4178,4278/Binding site: carbohydrate (Asn) #status predicted
F;168,2995/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
  urokinase-type
Ç;Species: Mus
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Species:
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Best Local
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;2772-2810/Domain:
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;2560-2594/Domain:
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                                                                                                                                                                                                                                                                                                                                   Matches
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Jomain: LDL receptor lly...

Jomain: LDL receptor llgand-bindiny

//Domain: LDL receptor llgand-binding repeat

//Domain: LDL receptor llgand-binding repeat hom...

//POmain: LDL receptor llgand-binding repeat homology

//Domain: LDL receptor llgand-binding repeat homology

//POmain: LDL receptor YMTD-containing repeat homology <YW40>

//BOMMAIN: LDL receptor YMTD-containing repeat homology <YW41>

//BOMMAIN: LDL receptor YMTD-containing repeat homology <YW41>

//BOMMAIN: LDL receptor YMTD-containing repeat homology <YW41>

//BOMMAIN: LDL receptor YMTD-containing repeat homology <YW42>

//BOMMAIN: LDL receptor YMTD-containing repeat homology <YW43>

//BOMMAIN: LDL receptor YMTD-containing repeat homology <YW43>

//POmmain: LDL receptor YMTD-containing repeat homology <YW44>

//POMMAIN: LDL receptor YMTD-containing repeat homology <YW44>

//POMMAIN: LDL receptor YMTD-containing repeat homology <YW44>

//POMMAIN: LDL receptor YMTD-containing repeat homology <YW45>

//POMMAIN: LDL receptor YMTD-containing repeat homology <YW45>
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urokinase-type plasminogen activator receptor men N;Alternate names: urokinase-type plasminogen act C;Species: Mus musculus (house mouse) C;Date: 06-Feb-1995 #sequence_revision 06-Feb-199 C;Accession: A55356; A41643 R;Suh, T.T.; Nerlov, C.; Dano, K.; Degen, J.L. J. Biol. Chem. 269, 25992-25998, 1994 A;Title: The murine urokinase-type plasminogen ac A;Feference number: A55356; MUID:95014420; PMID:7,Accession: A55356
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A;Title: The murine urokinase-type plasminogen activator A;Reference number: A55356; MUID:95014420; PMID:7929309 A;Accession: B55356
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C;Accession: B55356
R;Suh, T.T.; Nerlov, C.; Dano, K.; Degen, J.L.
J. Biol. Chem. 269, 25992-25998, 1994
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C;Species
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R;Kristensen, P.; Eriksen, J.; Blasi, F.; Dano, K. J. Cell Biol. 115, 1763-1771, 1991  
A;Title: Two alternatively spliced mouse urokinase receptor A;Reference number: A41643; MUID:92098587; PMID:1661735  
A;Accession: B41643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Keywords: alternative splicing; F; 24-108/Domain: Ly-6 homology <L)
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A; Residues: 1-222 < SUH>
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A;Residues: 1-222 <KRI>
A;Cross-references: UNIPROT:P35457; GB:X62701; NID:g53277; PIDN:CAA44575.1; PID:g53278
F;24-108/Domain: Ly-6 homology <LY6>
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A;Cross-references: GB:S70635; NID:g545770; PIDN:AAB30120.1; PID:g545771
C;Superfamily: urokinase-type plasminogen activator receptor; Ly-6 homology
C;Keywords: blocked carboxyl end; glycoprotein; lipoprotein; phosphatidylinositol
P;1-20/Domain: signal sequence #status predicted <SIG-
P;21-300/Product: urokinase-type plasminogen activator receptor #status predicted
P;21-104/Domain: Ly-6 homology <LY6A>
P;113-201/Domain: Ly-6 homology <LY6B>
P;113-201/Domain: Ly-6 homology <LY6B>
P;209-296/Domain: Ly-6 homology <LY6C>
P;301-330/Domain: carboxyl-terminal propeptide #status predicted <CPRO>
P;209-79/Binding site: carbohydrate (Asn) (covalent) #status predicted
P;300/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Gly) (in matur
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A;Cross-references: UNIPROT:P35456; GB:U12235; NID:g555809; PIDN:AAB60484.1;
A;Cross-references: UNIPROT:P35456; GB:U12235; NID:g555809; PIDN:AAB60484.1;
A;Cristensen, P.; Eriksen, J.; Blasi, F.; Dano, K.
J. Cell Biol. 115, 1763-1771, 1991
J. Cell Two alternatively spliced mouse urokinase receptor mRNAs with differ A;Reference number: A41643; MUID:92098587; PMID:1661735
A;Accession: A41643
                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:Q05588; GB:L03545; NID:g163802; PIDN:AAA30802.1; R;Reuning, U.; Little, S.P.; Dixon, E.P.; Johnstone, E.M.; Bang, N.U. Thromb. Res. 72; S9-70, 1993
A;Title: Molecular cloning of cDNA for the bovine urokinase-type plasminogen A;Reference number: I46977; MUID:94167671; PMID:8122188
A;Reference number: I46977
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Araetzschmar, J.; Haendler,
Gene 125, 177-183, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 urokinase-type plasminogen activator receptor precursor - bovine C;Species: Bos primigenius taurus (cattle) C;Date: 31-Dec-1993 #sequence revision 06-Sep-1996 #text_change 09-Jul-2004 C;Accession: JN0561; I46977
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-327 < KRI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;Title: Bovine urokinase-type plasminogen activator and ;Reference number: JN0560; MUID:93216119; PMID:8385052
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                                                                        Matches
                                                                                            Query Match
Best Local
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Pred. No. 5.7;
11; Mismatches
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                                                                                                                  DB 1;
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A; Nicatuo. F----
A; Molecule type: DNA
A; Residues: 1-1391 <WIL>
A; Cross-references: UNIPROT: Q19021;
A; Cross-references: Clone E01G6
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A,Residues: 1-1111 <WIL>
A,Cross-references: UNIPROT:Q9XWD6; EMB A,Experimental source: clone Y47H9C C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein E01G6.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #t C;Accession: T20406
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A;Introns: 50/2; 84/2;
C;Superfamily: ankyrin
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A;Introns: 44/1; 84/3; 175/1; 389/2; 423/1; 501/1; 1358/1
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A; Accession: T20406
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                                         67 RATSCGLEEPVSYRGVTY------SLTINCCTGRLCNRA-PSSQTVGAT 108
                                                                                                                             17 TTGVKDCVFCELTDSMQCP-----GTYMHC-GDDEDCFTGHGVAPGTGPVINKGCL
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28.3%;
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24.3%; Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #text_change
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                                                                                                                                                                                                                    Length 1391;
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                                                                                                                                                                           Indels
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                                                                                                                                                                           Gape
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RESULT 15
S42152
                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNĀ
A;Residues: 1-94,'C',96-328 <RA2>
A;Residues: 18-94,'C',96-328 <RA2>
A;Cross-references: EMBL:X71898
C;Superfamily: urokinase-type plasminogen activator receptor; Ly-6 homology
F;118-206/Domain: Ly-6 homology <LY6>
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A;Cross-references: UNIPROT:P49616; EMBL:X71899; NID:g452782; PIDN:CAA50718.1; PID:g4527
A;Accession: S41085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Rabbani, S.A.; Rajwans, N.; Achbarou, A.; Murthy, K.K.; Goltzman, D. FEBS Lett. 338, 69-74, 1994
A;Title: Isolation and characterization of multiple isoforms of the rat urokinase recept A;Reference number: S41085; MUID:94139899; PMID:8307160
A;Accession: S42152
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         urinary plasminogen activator receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S42152; S41085
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T27283
R;Ainscough, R.
submitted to the EMBL Data Library, September 1999
A;Reference number: Z20336
A;Accession: T27283
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A;Molecule type: DNA
A;Residues: 1-1620 <WIL>
A;Cross-references: EMBL:ALL110498; NID:e1542303; PIDN:CAB54471.1; CESP:Y64G10A.f
A;Experimental source: clone Y64G10A
A;Experimental source: clone Y64G10A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Introns: 77/1; 116/1; 198/1; 282/1; 365/1; 425/1; 466/1; 548/1; 559/1; 601/1; 625/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: CESP: Y64G10A.f
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Best Local S
Matches 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1047 LFGAGCKGICSC-----QNGATCDSVTGSCECRPGWRGKKCDR 1084
320 RL 321
                                                122 RL 123
                                                                                                260 VRGCATASWCQGSHVADSFQTHVNLSISCCNGSGCNRPTGGAPGPGPAHLILIASLLLIL 319
                                                                                                                                                                                                     203 VLDLQSLPPNGF---QCYSCEGNSTFGCSYEESSFIDCRGPMNQCLEATGLDVLGNRSYT 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       999 ACAPGTFG-KDCSKKCDCADGMHCDPSDGECICPPGKKGHKC--DETCDSG-----
                                                                                                                                                62 NKGCLRATSCGLEEPVSYRGVTYSLTTNCCTGRLCNRAPSSQTVGATTSLALGLGMLLPP 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 VINKGCLRATSCGLEEPVSYRGVTYSLTTNCC-----TGRLCNR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 ALPPGTTGVKDC-VFCELTDSMQC-----PGTYMH-CGDDEDCFTGHGVAPGTGP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31; Conservative
                                                                                                                                                                                                                                                     7 LLLVMALPPGTTGVKDCVFCELTDSMQC---PGTYMHC-GDDEDCFTGHGV-APGTGPVI 61
                                                                                                                                                                                                                                                                                                           30;
                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                     11.4%; Score 78; DB ilarity 24.6%; Pred. No. 9.5; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.5%; Score 78.5; D
29.5%; Pred. No. 33;
tive 5; Mismatches
                                                                                                                                                                                                                                                                                                                              DB 2; Length 328; 9.5;
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Search completed: April 15, 2005, 14:04:25 Job time : 17 secs